

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:40:32 : Search time 18 2143 seconds
(without alignments)
56.562 Million cell updates/sec

Title: us-09-856-070-25

Perfect score: 23

Sequence: 1 MLRLQ 5

Scoring table:

BLOSUM62

Gap-p 10.0, Gap-ext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	23	100.0	25	6 Q9BGJ5	Q9BGJ5 macaca fasc
2	23	100.0	25	6 Q9BGJ4	Q9BGJ4 pygathrix n
3	23	100.0	170	17 Q9YGNR	Q9YGNR aeropyrum p
4	23	100.0	143	10 Q9L1W4	Q9L1W4 oryza sativ
5	23	100.0	151	4 Q9P0NC	Q9P0NC homo sapien
6	23	100.0	156	4 Q9UJZ8	Q9UJZ8 homo sapien
7	23	100.0	157	17 Q9B576	Q9B576 archaetoglob
8	23	100.0	158	4 Q9UJZ7	Q9UJZ7 homo sapien
9	23	100.0	159	4 Q9UJZ6	Q9UJZ6 homo sapien
10	23	100.0	161	4 Q9UK20	Q9UK20 homo sapien
11	23	100.0	168	10 Q9LR06	Q9LR06 arabidopsis
12	23	100.0	173	10 Q9FJP3	Q9FJP3 arabidopsis
13	23	100.0	195	4 Q8WV17	Q8WV17 homo sapien
14	23	100.0	196	10 Q949T5	Q949T5 arabidopsis
15	23	100.0	196	13 Q9QY08	Q9QY08 ictalurus p
16	23	100.0	220	16 Q9Y870	Q9Y870 listeria in

ALIGNMENTS

RESULT 1

Q9BGJ5 Q9BGJ5 PRELIMINARY; PRT; 25 AA.
 AC Q9BGJ5; (1FMMHIREL, 17, Created)
 DT 01-JUN-2001 (1FMMHIREL, 17, last sequence update)
 DT 01-JUN-2001 (1FMMHIREL, 19, last annotation update)
 DE ATP synthase beta subunit (Fragment).
 OS Macaca fascicularis (Crab-eating macaque) (Cynomolous monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 PP SEQUENCE FROM N A
 RX MEDLINE=J100352; PubMed=11156956;
 RA Schmitz J., Olan M., Zischler H.;
 RI "LINE Insertions in Cladistic Analyses and the Phylogenetic
 RI Affiliations of Tarsius bancanus to Other Primates.*";
 RL Genetics 157:777-784(2001).
 DR EMBL; AF278735; AAK13310.1;
 FT NON_TER 1 1
 FT NON_TER 25 25
 SQ SEQUENCE 25 AA; 2957 Mw; 4FHRL14C73A6A4w CMC64;

Query Match: 100.0%; Score 23; DB 6; Length 25;
 Best Local Similarity: 100.0%; Pred. No. 25;
 Matches: 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 1 MLRLQ 5
 |||||
 Db 18 MLRLQ 22

RESULT 2

Q9BGJ4 Q9BGJ4 PRELIMINARY; PRT; 25 AA.
 AC Q9BGJ4;
 DT 01-JUN-2001 (1FMMHIREL, 17, Created)

Q9Y870 listeria mo
 Q9H611 homo sapien
 Q9ZD57 listeria in
 Q9Y869 listeria mo
 Q9ZQ15 rhizobium m
 Q9B28 xylella las
 Q9B32 brucella me
 Q85118 rhodobacter
 Q93576 rhodobacter
 Q9112 talstonia s
 Q94622 trypanosoma s
 Q98M86 rhizobium l
 Q9KQ17 bacillus ha
 Q9AG34 caulobacter
 Q9F416 pseudomonas
 Q9VW67 drosophila
 Q9Z661 rhizobium m
 Q9U19 agrobacteri
 Q9A865 escherichia
 Q9HX78 homo sapien
 Q98364 methanococ
 Q9VHK3 rattus norv
 Q957X1 schizosacch
 Q9N102 eptaleetus
 Q9NDK8 leishmania
 Q98D21 yersinia pe
 Q98D12 rhizobium l
 Q97TS2 clostridium
 Q9NKM3 leishmania

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DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ATP synthase beta subunit (Fragment).
OS Pyruvate dehydrogenase (E2) subunit.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54143;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 21160452; PubMed 11156996;
RA Schmitz J., Olm M., Zischner H.,
RI "SINE insertions in clades of Acanthaceae and the phylogenetic
RT Affiliations of various barcodes to other Primates."
RL GenBank 157:777-784(2001).
DR EMBL: AF278736; AAK14311.1;
KW Nucleotide.
FT Nucleotide
SQ SEQUENCE 25 AA: 2957 MW: 40860144C74A6A4B CRC64;
Query Match 100.0%; Score 23; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
DB 18 MLRLQ 22

RESULT 3
QYQY98 PRELIMINARY: PRT: 120 AA.
AC QYQY98;
DI 01-NOV-1999 (TrEMBLrel. 12, Created)
DI 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein: APE2250.
GN APE2250.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 99410439; PubMed 10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Naikawa Y.,
RA Jin no K., Takahashi M., Sekino M., Baba S.-I., Aikai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA RES. 6:83-103(1999).
DR EMBL: AF000064; AAK1262.1;
DR EMBL: AF000064; AAK1262.1;
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 120 AA: 13378 MW: 80662538D542F9B CRC64;
Query Match 100.0%; Score 23; DB 17; Length 120;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
DB 1 MLRLQ 5

RESULT 4
QYLIW4 PRELIMINARY: PRT: 133 AA.
AC QYLIW4;
DI 01-OCT-2000 (TrEMBLrel. 15, Created)

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DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Hypothetical 14.4 kDa protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX Using Y.C., Chow T., Chen C., Wu H., Chu M., Chao Y., Liu S.;
RI "Oryza sativa PAC10699E04 genomes sequence, complete sequence."
RT Submitted (JAN 2002) to the EMBL/GenBank/TrEMBL databases.
DR EMBL: AF001111; AAY0505.1;
KW Hypothetical protein.
SQ SEQUENCE 133 AA: 14391 MW: 63878295E6E32F3 CRC64;
Query Match 100.0%; Score 23; DB 10; Length 133;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
DB 108 MLRLQ 112

RESULT 5
QYQ9N0 PRELIMINARY: PRT: 151 AA.
AC QYQ9N0;
DI 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HSPC249.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-UMBILICAL CORD BLOOD;
RX MEDLINE 20499367; PubMed 11042152;
RA Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
RA Shen Y., Fan H.Y., Tu G., Cheng M., Xu X.F., Han Z.G., Zhang J.W.,
RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 309 previously unidentified genes expressed in CD34+ hematopoietic
RT stem/progenitor cells."
RL Genome RES. 10:1545-1550(2000).
DR EMBL: AF151083; AAF46169.1;
DR InterPro: IPR00517; Ribosomal_L30.
DR Pfam: PF00327; Ribosomal_L30; 1.
SQ SEQUENCE 151 AA: 17499 MW: 9DA686C92D100C64 CRC64;
Query Match 100.0%; Score 23; DB 4; Length 151;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
DB 1 MLRLQ 5

RESULT 6
QYQJZ8 PRELIMINARY: PRT: 156 AA.
AC QYQJZ8;
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheraia, Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RE TISSUE-BRAIN;
 KA Chen Z.C., Fadiel A., Naftolin F.,
 KL "Mutation of estrogen gene in cancer";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DT EMBL: AF188896; AAF03154.1; -
 DP InterPro: IPR000299; Band_4.1;
 DR InterPro: IPR000798; E2/7ad/moesin
 DR Pfam: PF00769; ERM; 1;
 DR PROSITE: PSS0057; BAND_41_3; 1;
 FT NON_TER 1 1
 FT NON_TER 156 156
 SQ SEQUENCE 156 AA; 19642 MW; 150PFAA684A203A6 CRC64.

Query Match: 100.0%; Score 23; DB 4; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
 DB 152 MLRLQ 156

RESULT 7
 ID 028576 PRELIMINARY; PRT: 157 AA.
 AC 028576;
 DT 01-JAN-1998 (TREMREL. 05, Created)
 DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
 DT 01-MAR-2002 (TREMREL. 20, Last annotation update)
 DE Hypothetical protein AF1697.
 GN AF1697.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton K.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Swinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kertavage A.P., Graham D.E., Kyriakides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty H.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.L., McNeil L.K., Budge J.H., Glodek A., Zhou L.,
 RA Overbeck R., Gonyne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Arlacher P., Kaine B.P., Sykes S.M.,
 RA Sadw P.W., Andrews K.P., Rowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RA "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997)
 CC - SIMILARITY: BELONGS TO THE ARSP FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: AF004486; AAF04557;
 DR TIGR: AF1697;
 DR InterPro: IPR001845; HTH_Arsk.
 DR Pfam: PF01022; HTH_5; 1;
 DR SMART: SM00418; HTH_Arsk; 1;
 KW DNA binding, Hypothetical protein, Transcription regulation,
 KW Complete proteome.
 SQ SEQUENCE 157 AA; 17478 MW; A00A270C7A7A6F9 CRC64;

Query Match: 100.0%; Score 23; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5

DB 94 MLRLQ 98

RESULT 8
 ID 090JZ7 PRELIMINARY; PRT: 158 AA.
 AC 090JZ7;
 DT 01-MAY-2000 (TREMREL. 13, Created)
 DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
 DT 01-MAY-2002 (TREMREL. 20, Last annotation update)
 DE Ezrin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=OVARY;
 RA Chen Z.C., Fadiel A., Naftolin F.;
 RL "Ezrin gene mutation in ovarian cancer";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DT EMBL: AF188897; AAF03155.1; -
 DR InterPro: IPR000299; Band_4.1;
 DR InterPro: IPR000798; E2/7ad/moesin.
 DR Pfam: PF00769; ERM; 1;
 DR PROSITE: PSS0057; BAND_41_3; 1;
 FT NON_TER 1 1
 FT NON_TER 158 158
 SQ SEQUENCE 158 AA; 19086 MW; 86192FHC6F2457E CRC64;

Query Match: 100.0%; Score 23; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
 DB 151 MLRLQ 155

RESULT 9
 ID 090JZ6 PRELIMINARY; PRT: 159 AA.
 AC 090JZ6;
 DT 01-MAY-2000 (TREMREL. 13, Created)
 DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
 DT 01-MAY-2002 (TREMREL. 20, Last annotation update)
 DE Ezrin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP Fadiel A., Chen Z.C., Naftolin F.;
 RL "Mutation of ezrin gene in cancer";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DT EMBL: AF188898; AAF03156.1; -
 DR InterPro: IPR000299; Band_4.1;
 DR InterPro: IPR000798; E2/7ad/moesin.
 DR Pfam: PF00769; ERM; 1;
 DR PROSITE: PSS0057; BAND_41_3; 1;
 FT NON_TER 1 1
 FT NON_TER 159 159
 SQ SEQUENCE 159 AA; 19244 MW; 7234848B7EA7A7A CRC64;

Query Match: 100.0%; Score 23; DB 4; Length 159;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRLQ 5
 DB 151 MLRLQ 155

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RESULT 10
Q9UKZ0 PRELIMINARY; PROT; 161 AA.
CT Q9UKZ0;
UT 01-MAY-2000 (TrEMBLrel_14, Created)
DT 01-MAY-2000 (TrEMBLrel_15, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel_20, Last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Khan Z.C., Fadiel A., Natoliin F.;
RT *Mutation analysis of ezrin gene in cancer cells.*;
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
DR EMBL; AF187552; AAC56713.1; -.
DR InterPro; IPR000294; Band_4.1.
DR InterPro; IPR000798; Pz/Pad/moslin.
DR Pfam; PF00373; Band_41; 1.
DR Pfam; PF00769; ERM; 1.
DR PROSITE; PS50057; BAND_41_3; 1.
FT NON_TER 1
FT NON_TER 161
SQ SEQUENCE 161 AA; 1943 MW; 5FD6E9B10E017099 CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 4; Length 161;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLQ 5
DB 157 MRLQ 161

RESULT 11
Q9UK06 PRELIMINARY; PROT; 168 AA.
CT Q9UK06;
UT 01-OCT-2000 (TrEMBLrel_15, Created)
DT 01-OCT-2000 (TrEMBLrel_15, Last sequence update)
DI 01-JUN-2001 (TrEMBLrel_17, Last annotation update)
DE Flua5.14.
OS Arabidopsis thaliana (Mouse ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
NC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC Rosales II; Brassicales; Brassicaceae; Arabidopsids.
NX NCBI_TaxID=3702;
RN [1]
RS SEQUENCE FROM N.A.
RC Check R., Shino P., Brooks S., Ruehler F., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altati B., Bei B., Chin C., Chion J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Leng C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Tortum M., Vayshberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Becker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
[2]
RN [2]
RS SEQUENCE FROM N.A.
RC Check R., Shino P., Brooks S., Ruehler F., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altati B., Bei B., Chin C., Chion J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Leng C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Tortum M., Vayshberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Becker J.;
RL Submitted (JUL-2000) To the
EMBL; AC006434; AAC87113.1; -.

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DR InterPro: IPR004029; S1.
DR SMART: SM00316; S1; 1.
SQ SEQUENCE 168 AA: 19121 MW: 4945484590HC5 CRC64:

Query Match 100.0%; Score 23; DB 10; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MURLO 5
IIIII
Db 118 MURLO 122

RESULT 12
Q9FJF3
ID Q9FJF3 PRELIMINARY; PRT; 173 AA.
AC Q9FJF3;
DT 01-WAR-2001 (TREMBLrel. 16, Created)
DI 01-WAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 50S ribosomal protein L29 (Putative 50S ribosomal protein L29).
CN AT5G56220.
OS Arabidopsis thaliana (Mouse ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid 1; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID:3702;
RN 111
RP SEQUENCE FROM N.A.
RA STRAIN=COLUMBIA;
RC MEDLINE=98404684; PubMed-9734815;
PA Kotachi H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RA "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RA Sequence features of the regions of 1,367,185 bp covered by 19
RA physically assigned pl and TAC clones.";
RA DNA Res. 5:203-216(1998).
RN 121
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Hanh J., Dale J.M., Goldsmith A.D.,
RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.H., Tang C., Toriumi M.,
RA Yamamura Y., Yu G., Yu S., Jones L., Carninci P., Chen H., Cheuk K.,
RA Hayashizaki Y., Ishida J., Bowser T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Tracy S.F., Shinozaki K., Davis K.W.,
RA Ecker J.R., Theologis A.;
RA "Full length cDNA of gene MN23-16/AT5g45220 (GI:10178184).";
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN 131
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Hanh J., Ptou P., Lee J.M.,
RA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;
RA "Arabidopsis Open Reading Frame (ORF) clones.";
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN 141
DR EMBL: AH013395; BAB11658.1; -;
DR EMBL: AY045966; AAK76640.1; -;
DR EMBL: AY079351; ANL95082.1; -;
DR InterPro: IPR001854; Ribosomal_L29.
DR Pfam: PF00431; Ribosomal_L29; 1.
DR TIGRfam: TIGR00012; L29; 1.
KW Ribosomal protein.
SQ SEQUENCE 173 AA: 19377 MW: 42046FC9464342 CRC64;

Query Match 100.0%; Score 23; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MURLO 5
IIIII
Db 91 MURLO 95

DR InterPro: IPR004029; S1.
DR SMART: SM00316; S1; 1.
SQ SEQUENCE 168 AA: 19121 MW: 4945484590HC5 CRC64:

Query Match 100.0%; Score 23; DB 10; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MURLO 5
IIIII
Db 118 MURLO 122

RESULT 12
Q9FJF3
ID Q9FJF3 PRELIMINARY; PRT; 173 AA.
AC Q9FJF3;
DT 01-WAR-2001 (TREMBLrel. 16, Created)
DI 01-WAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 50S ribosomal protein L29 (Putative 50S ribosomal protein L29).
CN AT5G56220.
OS Arabidopsis thaliana (Mouse ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid 1; Brassicales; Brassicaceae; Arabidopsis.
OC NCHI_TaxID-3702;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RC MEDLINE-98404684; PubMed-9734815;
PA Kotachi H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,167,185 bp covered by 19
RT physically assigned pl and TAC clones.";
RL DNA Res. 5:203-216(1998).
RN 121
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Pham P.K., Hanh J., Dale J.M., Goldsmith A.D.,
RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.H., Tang C., Toriumi M.,
RA Yamamura Y., Yu G., Yu S., Jones L., Carninci P., Chen H., Cheuk K.,
RA Hayashizaki Y., Ishida J., Bowser T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Tracy S.F., Shinozaki K., Davis K.W.,
RA Ecker J.R., Theologis A.;
RT "Full length cDNA of gene MN23-16/AT5g45220 (GI:10178184).";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN 131
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Hanh J., Ptou P., Lee J.M.,
RA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
RA Southwick A., Davis K.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) clones.";
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AH013395; BAB11658.1; -;
RL EMBL: AY045966; AAK76640.1; -;
RL EMBL: AY079351; ANL95082.1; -;
DR InterPro: IPR001854; Ribosomal_L29.
DR Pfam: PF00431; Ribosomal_L29; 1.
DR TIGRfams: TIGR00012; L29; 1.
KW Ribosomal protein.
SQ SEQUENCE 173 AA: 19477 MW: 421046FC9464342 CRC64;

Query Match 100.0%; Score 23; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MURLO 5
IIIII
Db 91 MURLO 95

RESULT 13

Q8WV17 PRELIMINARY: PPT: 195 AA.
 AC Q8WV17; 2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Similar to hypothetical protein FLJ22692.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Strausberg R.;
 EL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
 DR EMBL; BC018978; AAH18478.1; -;
 KW Hypothetical protein
 SQ SEQUENCE 195 AA: 21312 MW: 019719FF0GAR218 CR64;

Query Match 100.0%; Score 23; DB 4; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.6e-02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
 DQ 54 MLRQ 58

RESULT 14

Q949T5 PRELIMINARY: PPT: 196 AA.
 AC Q949T5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 22.3 kDa protein.
 GN F10A5.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Hanh J., Hanno P., Dale J.M.,
 RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
 RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
 RA Shinozaki K., Davis P.W., Ecker J.R., Theologis A.;
 RT *Full Length cDNA of gene F10A5.14 (GI:9369364).
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY050494; AAK43576.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 196 AA: 22258 MW: DFBH2571F9457HEC CR64;

Query Match 100.0%; Score 23; DB 10; Length 196;
 Best Local Similarity 100.0%; Pred. No. 1.6e-02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
 DQ 146 MLRQ 150

RESULT 15

Q90YU8

Q90YU8 PRELIMINARY: PPT: 196 AA.
 AC Q90YU8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Ribosomal protein L19.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Patterson A.P., Karsi A., Liu Z.J.;
 RT "Translational machinery of channel catfish: II. Complementary DNA and
 RL Submited (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF401574; AAK95146.1; -;
 EL InterPro: IPR006146; Pfam: PF01280; Ribosomal_L19e; 1;
 DR Pfam: PF01280; Ribosomal_L19e; 1;
 LP PPSITE: PS00526; PIRISOMAL_L19e; UNKNOWN.1.
 SQ SEQUENCE 196 AA: 23424 MW: 77EED1610E16EBC CR64;

Query Match 100.0%; Score 23; DB 13; Length 196;
 Best Local Similarity 100.0%; Pred. No. 1.6e-02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRQ 5
 DQ 3 MLRQ 7

Search completed: January 16, 2003, 16:55:47

Job time : 20.2143 secs

